
Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: markspencer

Timestamp: Mon Sep 10 13:56:07 EDT 2007

Validated By CRFValidator v 1.0.3

Application No: 10598965 Version No: 3.0

Input Set:

Output Set:

Started: 2007-08-21 16:34:39.997

Finished: 2007-08-21 16:34:40.432

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 435 ms

Total Warnings: 6

Total Errors: 0

No. of SeqIDs Defined: 7

Actual SeqID Count: 7

Error code	Error Description											
W 213	Artificial or Unknown found in <213> in SEQ ID (2)											
W 213	Artificial or Unknown found in <213> in SEQ ID (3)											
W 213	Artificial or Unknown found in <213> in SEQ ID (4)											
W 213	Artificial or Unknown found in <213> in SEQ ID (5)											
W 213	Artificial or Unknown found in <213> in SEQ ID (6)											
W 213	Artificial or Unknown found in <213> in SEQ ID (7)											

SEQUENCE LISTING

<110> Wei, Xin Gariepy , Jean <120> LIBRARY OF HETEROMERIC TOXIN MUTANTS, AND METHODS OF USING SAME <130> 34104-0082 <140> 10598965 <141> 2007-08-21 <160> 7 <170> PatentIn version 3.2 <210> 1 <211> 299 <212> PRT <213> Escherichia coli <220> <221> misc_feature <223> Wild type SLT-1 A chain <400> 1 Ile Glu Gly Arg Ala Ser Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala 10 15 1 Lys Thr Tyr Val Asp Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr 25 30 20 Pro Leu Gln Thr Ile Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp 35 40 45 Ser Gly Ser Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp 50 55 60 Pro Glu Glu Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn 65 70 75 80 Asn Leu Tyr Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr 85 90 95 Arg Phe Ala Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val 100 105 110

Thr Leu Ser Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly

115 120 125

Ile Ser Arg Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser 130 135 140

Tyr Leu Asp Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val 145 150 150

Ala Arg Ala Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg

165

170

175

Phe Arg Gln Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser 180 185

Gly Arg Ser Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn 195 200 205

Trp Gly Arg Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser 210 215 220

Val Arg Val Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly 225 230 230 240

Ser Val Ala Leu Ile Leu Asn Cys His His Ala Ser Arg Val Ala
245
250
255

Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro Ala Asp Gly Arg 260 265 270

Val Arg Gly Ile Thr His Asn Lys Ile Leu Trp Asp Ser Ser Thr Leu 275 280 285

Gly Ala Ile Leu Met Arg Arg Thr Ile Ser Ser 290 295

<210> 2

<211> 32

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 2

```
<210> 3
<211>
       31
<212>
      DNA
<213> Artificial
<220>
<223> Primer
<400> 3
                                                                      31
gagaagaaga gactgcagat tccatctgtt g
<210> 4
<211> 302
<212>
      PRT
<213> Artificial
<220>
       SLT-1 A Chain lib#3 protein sequence (SAM3)
<223>
<400> 4
Lys Gly Met Arg Ser His His His His His His His Ile Glu Gly
                5
                                    10
                                                        15
1
Arg Ala Ser Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr
            20
                                25
                                                    30
Val Asp Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln
        35
                            40
                                                45
Thr Ile Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Ser
                        55
    50
                                            60
Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu
65
                                        75
                                                            80
                    70
Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr
                85
                                    90
                                                        95
Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala
            100
                                105
                                                    110
Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser
        115
                            120
                                                125
```

Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg

130 135 140

Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp
145 150 155 160

Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala

165
170
175

Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln
180 185 190

Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser 195 200 205

Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg 210 215 220

Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val 225 230 230 235 240

Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala
245 250 255

Leu Ile Leu Asn Cys His His His Ile Tyr Ser Asn Lys Leu Met Ala 260 270

Ser Arg Val Ala Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro 275 280 285

Ala Asp Gly Arg Val Arg Gly Ile Thr His Asn Lys Ile Leu 290 295 300

<210> 5

<211> 319

<212> PRT

<213> Artificial

<220>

<223> SLT-1 A Chain lib#5 protein sequence (SAM5)

<400> 5

Lys Gly Met Arg Ser His His His His His His His His Ile Glu Gly

1 10 15

Arg	Ala	Ser	Lys 20	Glu	Phe	Thr	Leu	Asp 25	Phe	Ser	Thr	Ala	Lys 30	Thr	Tyr
Val	Asp	Ser 35	Leu	Asn	Val	Ile	Arg 40	Ser	Ala	Ile	Gly	Thr 45	Pro	Leu	Gln
Thr	Ile 50	Ser	Ser	Gly	Gly	Thr 55	Ser	Leu	Leu	Met	Ile 60	Asp	Ser	Gly	Ser
Gly 65	Asp	Asn	Leu	Phe	Ala 70	Val	Asp	Val	Arg	Gly 75	Ile	Asp	Pro	Glu	Glu 80
Gly	Arg	Phe	Asn	Asn 85	Leu	Arg	Leu	Ile	Val 90	Glu	Arg	Asn	Asn	Leu 95	Tyr
Val	Thr	Gly	Phe 100	Val	Asn	Arg	Thr	Asn 105	Asn	Val	Phe	Tyr	Arg 110	Phe	Ala
Asp	Phe	Ser 115	His	Val	Thr	Phe	Pro 120	Gly	Thr	Thr	Ala	Val 125	Thr	Leu	Ser
Gly	Asp 130	Ser	Ser	Tyr	Thr	Thr 135	Leu	Gln	Arg	Val	Ala 140	Gly	Ile	Ser	Arg
Thr 145	Gly	Met	Gln	Ile	Asn 150	Arg	His	Ser	Leu	Thr 155	Thr	Ser	Tyr	Leu	Asp 160
Leu	Met	Ser	His	Ser 165	Gly	Thr	Ser	Leu	Thr 170	Gln	Ser	Val	Ala	Arg 175	Ala
Met	Leu	Arg	Phe 180	Val	Thr	Val	Thr	Ala 185	Glu	Ala	Leu	Arg	Phe 190	Arg	Gln
Ile	Gln	Arg 195	Gly	Phe	Arg	Thr	Thr 200	Leu	Asp	Asp	Leu	Ser 205	Gly	Arg	Ser
Tyr	Val 210	Met	Thr	Ala	Glu	Asp 215	Val	Asp	Leu	Thr	Leu 220	Asn	Trp	Gly	Arg
Leu 225	Ser	Ser	Val	Leu	Pro 230	Asp	Tyr	His	Gly	Gln 235	Asp	Ser	Val	Arg	Val 240

Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala

245 250 255

Leu Ile Leu Asn Cys His His His Ala Ala Phe Ala Asp Leu Ile Ala 260 270

Ser Arg Val Ala Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro 275 280 285

Ala Asp Gly Arg Val Arg Gly Ile Thr His Asn Lys Ile Leu Trp Asp 290 295 300

Ser Ser Thr Leu Gly Ala Ile Leu Met Arg Arg Thr Ile Ser Ser 305 310 315

<210> 6

<211> 7

<212> PRT

<213> Artificial

<220>

<223> First melanoma active insert

<400> 6

Ile Tyr Ser Asn Lys Leu Met
1 5

<210> 7

<211> 7

<212> PRT

<213> Artificial

<220>

<223> Second melanoma active insert

<400> 7

Ala Ala Phe Ala Asp Leu Ile 1 5